



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/732,476A

Source: OIPE

Date Processed by STIC: 6/20/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/237,476A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) SS missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 06/20/2001

PATENT APPLICATION: US/09/737,476A

TIME: 14:38:23

Input Set : A:\09737476.txt

Output Set: N:\CRF3\06202001\I737476A.raw

Does Not Comply
Corrected Diskette Needed

P.6

3 <110> APPLICANT: Leo G.J. FRENKEN
 4 Cornelis P.E. van der LOGT
 5 Vin-Miin TEH
 6 Martine E. VERHOEYEN
 7 Joy E. WILKINSON
 8 Stephen A. JOBLING
 10 <120> TITLE OF INVENTION: Production of Antibodies
 12 <130> FILE REFERENCE: 060113/0275850 - T7060C
 14 <140> CURRENT APPLICATION NUMBER: US 09/737,476A
 16 <141> CURRENT FILING DATE: 2000-12-18
 18 <150> PRIOR APPLICATION NUMBER: EP 99310188.0
 20 <151> PRIOR FILING DATE: 1999-12-17
 22 <160> NUMBER OF SEQ ID NOS: 67
 23 <170> SOFTWARE: MS Word
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 440
 27 <212> TYPE: DNA
 C--> 28 <213> ORGANISM: Artificial
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 31 <223> OTHER INFORMATION: VHH with peptide linker
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (1)..(417)
 37 <400> SEQUENCE: 1
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 40 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 41 1 5 10 15
 43 tct ctg aga ctc tcc tgt gca gcc tcg gga cgc gcc acc agt ggt cat 96
 44 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 45 20 25 30
 47 ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag gag cgt 144
 48 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 49 35 40 45
 51 gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg tat aaa 192
 52 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 53 50 55 60
 55 gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc aag act 240
 56 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 57 65 70 75 80
 59 acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt 288
 60 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 61 85 90 95
 63 tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg 336
 64 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 65 100 105 110
 67 gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca 384
 68 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser

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Input Set : A:\09737476.txt

Output Set: N:\CRF3\06202001\I737476A.raw

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71 gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa      437
72 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
73      130          135
75 ttc      440
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79 <211> LENGTH: 139
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84 <400> SEQUENCE: 2
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89 1          5          10          15
91 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
92      20          25          30
94 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
95      35          40          45
97 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
98      50          55          60
100 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
101 65          70          75          80
103 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
104      85          90          95
106 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
107      100          105          110
109 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
110      115          120          125
112 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
113      130          135
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 11
118 <212> TYPE: PRT
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120 <220> FEATURE:
121 <223> OTHER INFORMATION: myc linker
122 <400> SEQUENCE: 3
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127 1          5          10
130 <210> SEQ ID NO: 4
131 <211> LENGTH: 471
132 <212> TYPE: DNA
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134 <220> FEATURE:
135 <223> OTHER INFORMATION: VHH with linker
136 <220> FEATURE:
137 <221> NAME/KEY: CDS
138 <222> LOCATION: (1)..(459)
139 <400> SEQUENCE: 4

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146 1          5          10          15
148 tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat      96
149 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
150          20          25          30
152 cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc      144
153 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
154          35          40          45
156 gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag      192
157 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
158          50          55          60
160 ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta      240
161 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
162 65          70          75          80
164 caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct      288
165 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
166          85          90          95
168 gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc      336
169 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
170          100          105          110
172 ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg      384
173 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
174          115          120          125
176 gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc      432
177 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
178          130          135          140
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182 145          150
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199          20          25          30
201 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
202          35          40          45
204 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
205          50          55          60
207 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
208 65          70          75          80
210 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
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Input Set : A:\09737476.txt

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213 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
214          100          105          110
216 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
217          115          120          125
219 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
220          130          135          140
222 Ser Glu Glu Asp Leu Asn Gly Ala Ala
223 145          150
226 <210> SEQ ID NO: 6
227 <211> LENGTH: 468
228 <212> TYPE: DNA
C--> 229 <213> ORGANISM: Artificial
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242 1          5          10          15
244 tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata      96
245 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
246          20          25          30
248 gct atg gcc tgg tac cgc cag gct cca ggg aag cag cgc gag gtg gtc      144
249 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
250          35          40          45
252 gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag      192
253 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
254          50          55          60
256 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg      240
257 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
258 65          70          75          80
260 caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct      288
261 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
262          85          90          95
264 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg      336
265 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
266          100          105          110
268 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc      384
269 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
270          115          120          125
272 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca      432
273 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
274          130          135          140
276 gaa gag gat ctg aat ggg gcc gca tagtaacaat tg      468
277 Glu Glu Asp Leu Asn Gly Ala Ala
278 145          150
281 <210> SEQ ID NO: 7

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/737,476A

DATE: 06/20/2001

TIME: 14:38:23

Input Set : A:\09737476.txt

Output Set: N:\CRF3\06202001\I737476A.raw

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282 <211> LENGTH: 152
283 <212> TYPE: PRT
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287 <223> OTHER INFORMATION: VHH with linker
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291 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
292 1 5 10 15
294 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
295 20 25 30
297 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
298 35 40 45
300 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
301 50 55 60
303 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
304 65 70 75 80
306 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
307 85 90 95
309 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
310 100 105 110
312 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
313 115 120 125
315 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
316 130 135 140
318 Glu Glu Asp Leu Asn Gly Ala Ala
319 145 150
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323 <211> LENGTH: 462
324 <212> TYPE: DNA
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327 <220> FEATURE:
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330 <220> FEATURE:
331 <221> NAME/KEY: CDS
332 <222> LOCATION: (1)..(450)
334 <400> SEQUENCE: 8
336 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag 48
337 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
338 1 5 10 15
340 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc 96
341 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
342 20 25 30
344 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt 144
345 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
346 35 40 45
348 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg 192
349 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
350 50 55 60
352 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac 240

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09/732,476A 6

<210> 55

<211> 377

<212> PRT

<213> Artificial

see item 11 on Euro Summary Sheet

<400> 55

Met Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly

VERIFICATION SUMMARY

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DATE: 06/20/2001

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Input Set : A:\09737476.txt

Output Set: N:\CRF3\06202001\I737476A.raw

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L:81 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:119 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:133 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:188 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:229 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/737,476A

DATE: 06/20/2001

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Input Set : A:\09737476.txt

Output Set: N:\CRF3\06202001\I737476A.raw

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L:1249 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1249 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: